



TABLE I

THE PERCENT IDENTITY OF DATABASE SEQUENCES TO SNORF72

NOTE: Each accession number was tested using the GAP algorithm of the human SNORF72 receptor sequence

NOTE: The nucleic acid sequence of hSNORF72 (SEQ ID NO:3) was used to perform GAPs on accessions from nucleic acid databases.

The amino acid sequence of hSNORF72 (SEQ ID NO:4) was used to perform GAPs on accessions from protein databases.

RECEPTOR NAME	DATABASE	ACCESSION	MATCH KIND	PERCENT GAP ID	RELEVANCE
hSNORF72	DERWENT GENE_N				
		AAZ33297	NUCLEIC	99.439	The SNORF72 sequence starts at position 65 of this sequence, there are 7 nucleotide mismatches.
		AAZ49707	NUCLEIC	59.983	This sequence matches SNORF62 receptor.
		AAZ49706	NUCLEIC	56.355	This sequence is a mouse homolog
		AAZ52992	PROTEIN	98.554	This sequence has 6 amino acid mismatches compared to SNORF72
	DERWENT GENE_P	AAZ44642	PROTEIN	47.68	This sequence matches SNORF62 receptor.
		AAZ44641	PROTEIN	45.407	This sequence is a mouse homolog
		AF044600	NUCLEIC	59.018	This sequence matches SNORF62 receptor.
		AF044601	NUCLEIC	57.292	This sequence matches SNORF62 receptor.
		AF044602	NUCLEIC	55.802	This sequence is a mouse homolog
HTG (GENEMBL)	SWISSPROT PLUS	O43664	PROTEIN	47.089	This sequence matches SNORF62 receptor.
		O55040	PROTEIN	45.407	This sequence is a mouse homolog
					This sequence matches SNORF62, the sequence is too large and that portion of sequence which matches SNORF62 was assembled and used for GAP.
		AC017104	NUCLEIC	58.148	
					The accession is too large, that portion of the sequence that matches the SNORF72 receptor was assembled used for GAP (from 104011-104736; 97683-97767; 95080-95204; 91814-92127 all match in reverse frame) there is 1 nucleotide mismatch at position 1183 of hSNORF72.
	EST	AC008571	NUCLEIC	99.92	
		AQ019411	NUCLEIC	100	Only a small portion-85 nucleotides, of this sequence (from position 221-305) is a 100% match to hSNORF72 (in reverse 811-727) the rest is genomic sequence.
		AQ015065	NUCLEIC	100	Only a small portion-85 nucleotides, of this sequence (from position 221-305) is a 100% match to hSNORF72 (in reverse frame 811-727) the rest is genomic sequence.
		AA562357	NUCLEIC	54.026	This sequence is a mouse homolog
		N45474	NUCLEIC	100	A portion of this sequence (from position 1-278) is 100% match to hSNORF72 (971-1248)
		H11359	NUCLEIC	100	A portion of this sequence (from position 269-379) is 100% match to hSNORF72 (727-837)
		R13353	NUCLEIC	83.465	A portion of this sequence (from position 284-424) matches our hSNORF72 (736-862)
		R13890	NUCLEIC	99.363	A portion of this sequence (from position 273-432) matches our hSNORF72 (727-883)